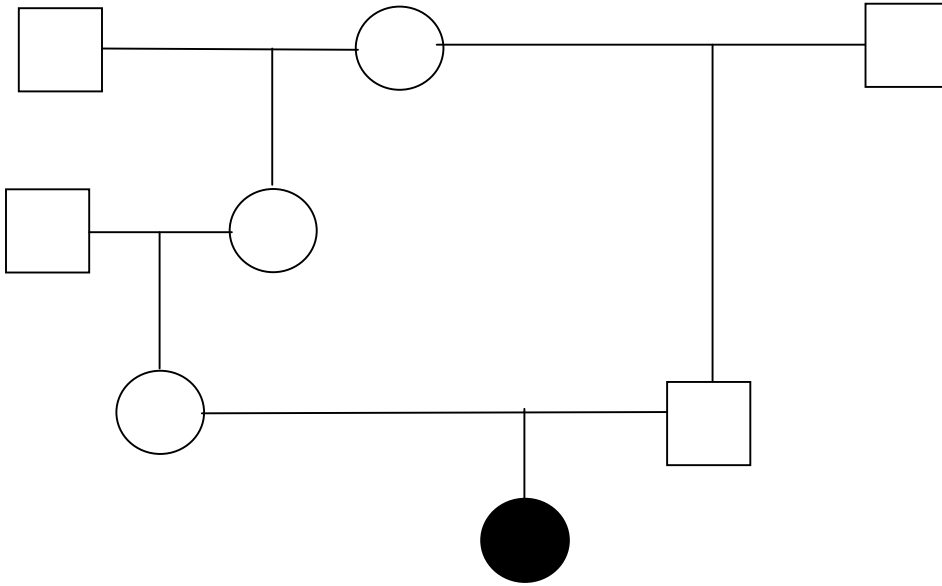
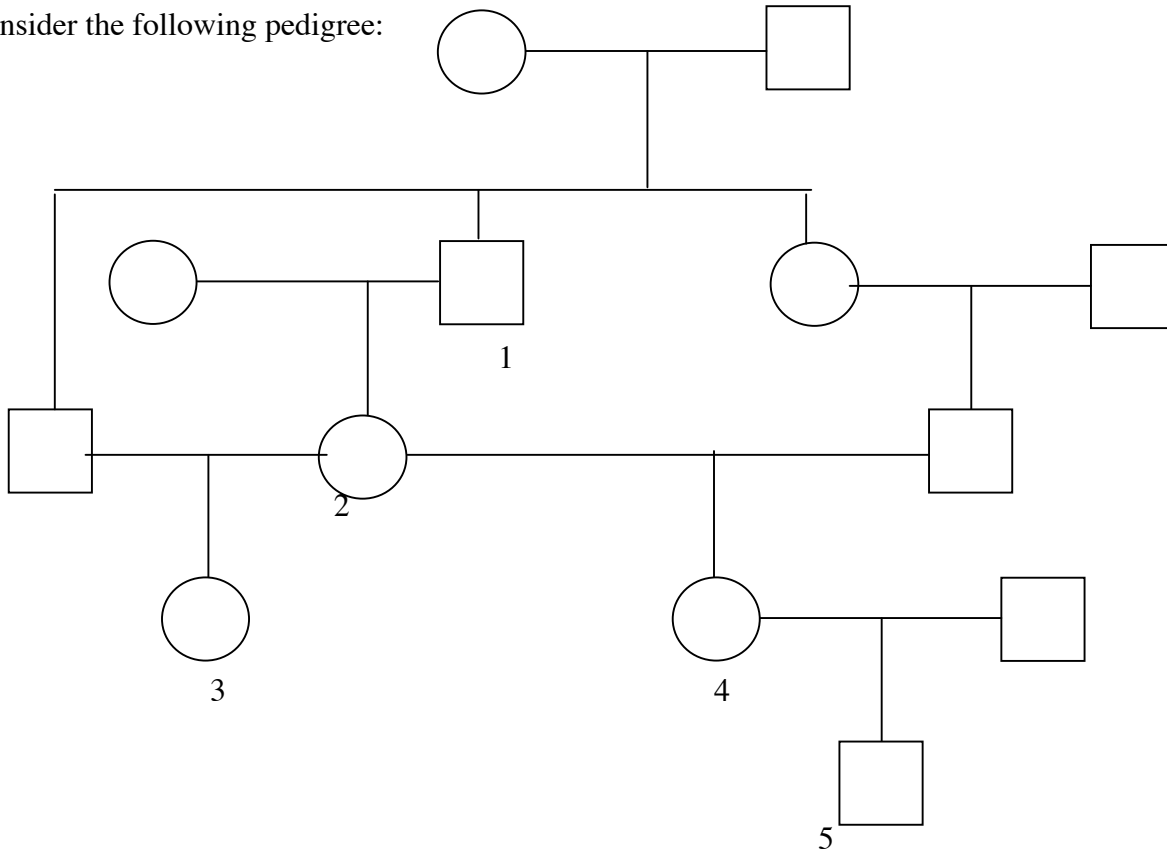


1. Consider the following pedigree:



- a). What is the pedigree inbreeding coefficient F of the female shown by the solid circle relative to this pedigree? **2 pts.**
- b). What is the probability of identity by descent in the female shown by the solid circle of a randomly chosen X-linked locus relative to this pedigree? **3pts.**

2. Consider the following pedigree:



Indicate which of the numbered individuals are inbred in the sense that $F > 0$ based on the information in the pedigree. **5pts.**

3. The incidence of an autosomal recessive genetic disease in a population is 1.2%. The frequency of the disease allele in the gene pool is 0.05. What is f for this population? **2 pts.**

4. Given the following allele frequencies for an autosomal locus with two alleles (A and a , with p being the frequency of A) and inbreeding coefficients (measured as a deviation from Hardy–Weinberg proportions in all problems in this set), calculate the genotype frequencies. **4 pts**

a. $p = 0.8, f = -0.2$

b. $p = 0.3, f = 0.5$

c. $p = 0.4, f = -0.3$

d. $p = 0.1, f = 0.9$

5. Consider the following three populations. For each population, estimate the value of f given the following genotype numbers. **3 pts.**

Genotypes	AA	Aa	aa
a.	25	50	25
b.	8	64	128
c.	49	42	9

Now assume that an investigator pooled all three samples together and regarded them as a single population. Estimate the value of f for the pooled sample and test the null hypothesis that $f = 0$ and use a p-level of 0.05 to accept or reject the null hypothesis. **6 pts.**

6. A population has variation at two loci, each with two alleles (A and a ; B and b) with a recombination frequency of 0.2 between the loci. The genotype frequencies are as follows:

Genotypes	AB/AB	AB/Ab	AB/aB	AB/ab	Ab/Ab	Ab/aB	aB/aB	Ab/ab	aB/ab	ab/ab
freq.	0.25	0.1	0.1	0.3	0.01	0.02	0.01	0.06	0.06	0.09

Assume now that each capital letter allele contributes +2 to a phenotype and each small letter allele contributes 0 to a phenotype, with the total phenotypic value determined by the sum of these numbers over both alleles and both loci.

Assume further that there is 100% assortative mating. What are the equilibrium genotype frequencies? **5 pts.**